

Pathway-Based Genome-Wide Association Studies for Two Meat Production Traits in Simmental Cattle

Huizhong Fan¹, Yang Wu¹, Xiaojing Zhou², Jiangwei Xia¹, Wengang Zhang¹, Yuxin Song¹, Fei Liu^{1,3}, Yan Chen¹, Lupei Zhang¹, Xue Gao¹, Huijiang Gao^{1*}, and Junya Li^{1*}

1. Institute of Animal Science, Chinese Academy of Agricultural Science, Beijing 100193, China
2. Department of Mathematics, Heilongjiang Bayi Agricultural University, 163319 Daqing, China
3. College of Animal Science and Technology, Agricultural University of Hebei Province, Baoding, 071001, China

*Corresponding author: Huijiang Gao. Email: gaohj111@sina.com

Junya Li. Email: JL1@iascaas.net.cn

Emails of the other authors:

Huizhong Fan: fanhuizhong1990@qq.com

Yang Wu: wuyangf7@126.com

Xiaojing Zhou: 964703463@qq.com

Jiangwei Xia: 290466673@qq.com

Wengang Zhang: 1015210729@qq.com

Yuxin Song: 2361278555@qq.com

Fei Liu: liufeiyjy@163.com

Yan Chen: chenyan0204@163.com

Lupei Zhang: lpzhang@iascaas.net.cn

Xue Gao: gaoxue76@126.com

Table S2: The result of significant pathways (P<0.01) discovered by Smallest P-value method and SSEA method.

Method	Trait	Pathway	Description	ES	NES	P value	FDR
Smallest P-value method	LW	bta04727	GABAergic synapse	0.35	2.76	1.121E-04	0.26
	LMA	bta04932	Non-alcoholic fatty liver disease (NAFLD)	0.30	3.16	1.837E-04	0.14
SSEA method	LW	bta04727	GABAergic synapse	0.38	2.99	3.061E-04	0.21
	LMA	bta04932	Non-alcoholic fatty liver disease (NAFLD)	0.35	3.47	2.177E-05	0.08
		bta04060	Cytokine-cytokine receptor interaction	0.30	2.53	7.533E-02	0.25

LW, live weight; LMA, longissimus muscle area. ES, enrichment score; NES, normalized enrichment score; FDR, false discovery rate.